

of the pea protein (AKFSRDS (SEQ ID NO: 37)). Because the proteins are so similar around this region it can be predicted that the mature terminus of the cassava SBE II protein is likely to be GKSSHES (SEQ ID NO: 38). The precursor has a predicted molecular mass of 96 kD and the mature protein a predicted molecule mass of 91.3 kD. The cassava SBE II has a short acidic tail at the C-terminal although this is not as long or as acidic as that found in the pea or potato proteins. The significance of this acidic tail, if any, remains to be determined. One notable difference between the amino acid sequence of cassava SBE II and all other SBE II proteins is the presence of the sequence NSKH (SEQ ID NO: 32) at around position 697 instead of the conserved sequence DAD/EY (SEQ ID NO: 33). Although this conserved region forms part of a predicted  $\alpha$ -helix (number 8) of the catalytic  $(\beta/\alpha)_8$  barrel domain (Burton et al 1995 cited previously), this difference does not abolish the SBE activity of the cassava protein as this gene can still complement the glycogen branching deletion mutant of *E. coli*. It may however affect the specificity of the protein. An interesting point is that the other cassava SBE II clone pSJ94 has the conserved sequence DADY (SEQ ID NO. 33).

Please delete the previous sequence listing on pages 24-50 and substitute therefore new pages 1-69 which comprise the paper copy of the corrected Sequence Listing and renumber them accordingly.

**In the abstract:**

Please replace the abstract with the replacement abstract submitted on the attached page:  
~~Disclosed is a nucleic acid sequence encoding a polypeptide having starch branching enzyme (SBE) activity, the encoded polypeptide comprising an effective portion of the amino acid sequence shown in Figure 4 (SEQ. ID. NO. 29) or Figure 13 (SEQ. ID. NO. 31).~~